



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/759,281

Source: OIPE

Date Processed by STIC: 1-29-01

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/759,281

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☒ Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length      Sequence(s) \_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES)      Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES)      Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☐ Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES)      Sequence(s) \_\_\_\_ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES)      Sequence(s) \_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

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Does Not Comply  
Corrected Diskette Needed

# SEQUENCE LISTING

## GENERAL INFORMATION:

(i) ← *move to same line*

APPLICANT: PEREGRINO FERREIRA, Paulo;

8 GESSIEN KROON, Erna;

PIMENTA DOS REIS, Karlisson Jennner;

BIAS FORTES FERRAZ, Isabella;

CERQUEIRA LEITE, Romulo.

(ii) ← *Same line*

10 TITLE OF INVENTION: Method and composition for the diagnosis of equine  
infectious anemia virus disease by using the recombinant capsid protein virus

(p26)

(iii) ← *Same line*

NUMBER OF SEQUENCES: 1

15 (iv) ←

CORRESPONDENCE ADDRESS:

(A) ←

ADDRESSEE: Universidade Federal de Minas Gerais - CTIT

(B) ←

20 STREET: Avenida Antônio Carlos, 6627 Bairro São Francisco

(C) ←

CITY: Belo Horizonte

(D) ←

STATE: Minas Gerais

25 (E) ←

COUNTRY: BRAZIL

(F) ←

ZIP: 31270-901

(v) ←

30 COMPUTER READABLE FORM:

(A)

\* *File not saved  
in ASCII text  
See # 5 on  
the Error Summary  
Sheet.*

↑  
Delete  
Numerals in  
the margin  
↓

*Move all  
response to  
where arrows  
indicate.*

*Example →*

(i) GENERAL INFORMATION:  
(ii) APPLICANT:  
(iii) TITLE OF INVENTION:  
(iv) NUMBER OF SEQUENCES:  
(v) CORRESPONDENCE ADDRESS:  
(vi) ADDRESSEE:  
(vii) STREET:  
(viii) CITY:  
(ix) STATE:  
(x) COUNTRY:  
(xi) ZIP:

(A) ←

MEDIUM TYPE: diskette – 3.50 inch, 1.44 Mb storage

(B) ←

COMPUTER: IBM compatible

(C) ←

8 OPERATING SYSTEM: Windows 98

(D) ←

SOFTWARE: Office premium

(vi) ←

CURRENT APPLICATION DATA:

(A) ← 09/759, 281

APPLICATION NUMBER: U.S. ~~09/331-262~~

(B) ←

FILING DATE:

(C) ←

15 CLASSIFICATION: C12Q1/70

(vii) ←

PRIOR APPLICATION DATA

(A) ←

APPLICATION NUMBER: PI 9606273-8

20 (B) ←

FILING DATE: 18-DEC-1996

(2) ←

INFORMATION FOR SEQ ID NO:1:

(i) ←

25 SEQUENCE CHARACTERISTICS:

(A) ←

LENGTH: 252 amino acids

(B) ←

TYPE: amino acid

30 (D) ←

TOPOLOGY: linear

Move all  
response to where  
arrows indicate.

(\*) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE:  
(B) COMPUTER:  
(C) OPERATING SYSTEM:  
(D) SOFTWARE:  
(\*) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:  
(\*) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(\*) ATTORNEY/AGENT INFORMATION:  
(A) NAME:  
(B) REGISTRATION NUMBER:  
(C) REFERENCE/DOCKET NUMBER:  
(\*) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE:  
(B) TELEFAX:  
(C) TELEX:

There are 321 amino acids  
shown see p 5

Delete  
the numerals  
in the margin

(ii) ←

MOLECULE TYPE : protein

(vi) ←

ORIGINAL SOURCE

(A) ←

ORGANISM : equine infectious anemia virus

(ix) ←

FEATURE:

(A) ←

NAME: p26

(x) ←

PUBLICATION INFORMATION

(A)

AUTHORS:

(B)

TITLE: (

C)

JOURNAL:

(D)

VOLUME:

(F)

PAGES:

(G)

DATE:

(xi) ←

SEQUENCE DESCRIPTION: SEQ ID NO:1

His His His His His His Gly Ser Pro Gly Asn Pro Leu Thr Trp

move responses to  
where arrows indicate.

2) INFORMATION FOR SEQ ID NO: X:  
 (1) SEQUENCE CHARACTERISTICS:  
   (A) LENGTH:  
   (B) TYPE:  
   (C) STRANDEDNESS:  
   (D) TOPOLOGY:  
 (2) MOLECULE TYPE:  
 (3) HYPOTHETICAL:  
 (4) ANTI-SENSE:  
 (5) FRAGMENT TYPE:  
 (6) ORIGINAL SOURCE:  
 (7) ORGANISM:

Do not include  
headings which have  
no response.

↑  
Delete  
numerals  
in the  
margin.

↓

Ser Lys Ala Leu Lys Lys Leu Glu Lys Val Thr Val Gln Gly Ser

20 25 30

Gln Lys Leu Thr Thr Gly Asn Cys Na Trp Ala Leu Ser Leu Val

35 40 45

5 Asp Leu Phe His Asp Thr Asn Phe Val Lys Glu Lys Asp Trp Gln

50 55 60

Leu Arg Asp Val Ile Pro Leu Leu Glu Asp Val Thr Gln Thr Val

65 70 75

Ser Gly Gln Glu Arg Glu Ala Phe Glu Arg Thr Trp Trp Ala Ile

80 85 90

Ser Ala Val Lys Met Gly Leu Gln Ile Asn AsnVal Val Asp Gly

95 100 105

Lys Ala Ser Phe Gln Leu Leu Arg Ala Lys Tyr Glu Lys Lys Thr

110 115 120

Ala Asn Lys Lys Gln Ser Glu Pro Ser Glu Glu Tyr Pro Ile Met

125 130 135

Ile Asp Gly Ala Gly Asn Arg Asn Phe Arg Pro Leu Thr Pro Arg

140 145 150

Gly Tyr Thr Thr Trp Val AsnThr Ile Gln Thr Asn Gly Leu Leu

155 160 165

Asn Glu Ala Ser Gln Asn Leu Phe Gly Ile Leu Ser Val Asp Cys

170 175 180

Thr Ser Glu Glu Met Asn Ala Phe Leu Asp Val Val Pro Gly Gln

185 190 195

25 Ala Gly Gln Lys Gln Ile Leu Leu Asp Ala Ile Asp Lys Ile Ala

200 205 210

Asp Asp Trp Asp Asn Arg His Pro Leu Pro Asn Ala Pro Leu Val

215 220 225

Ala Pro Pro Gln Gly Pro Ile Pro Met Thr Ala Arg Phe Ile Arg

230 235 240

Gly Leu Gly Val Pro Arg Glu Arg Gln Met Glu Pro

245 250

↑  
Delete  
numerals in  
the margin  
↓

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Asn Cys Val Val Gln Ser Phe Gly Val Ile Gly Gln Ala His Leu.

255? 260 265 270

Glu Leu Pro Arg Pro Asn Lys Arg Ile Arg Asn Gln. Ser Phe Asn

275 280 285

~~5~~ Gln Tyr Asn Cys Ser Ile Asn. Asn Lys Thr Glu Leu Glu Thr Trp

290 295 300

Lys Leu. Val Lys Thr Ser Gly Val Thr Pro Leu Pro. Ile Ser Ser

305 310 315

Glu Ala Asn Thr Gly Leu

~~10~~ 320